

Bluetongue Virus Serotype 1 Outbreak in the Basque Country (Northern Spain) 2007–2008. Data Support a Primary Vector Windborne Transport

Rodrigo García-Lastra¹, Iratxe Leginagoikoa¹, Jose M. Plazaola², Blanca Ocabo³, Gorka Aduriz¹, Telmo Nunes⁴, Ramón A. Juste^{1*}

1 Department of Animal Health, NEIKER-Tecnalia, Derio, Bizkaia, Spain, **2** Departamento de Desarrollo Rural, Diputación Foral de Gipuzkoa, Donostia, Gipuzkoa, Spain, **3** Departamento de Agricultura, Diputación Foral de Bizkaia, Bilbao, Bizkaia, Spain, **4** Faculdade de Medicina Veterinária, TU Lisbon, Lisbon, Portugal

Abstract

Background: Bluetongue (BT) is a vector-borne disease of ruminants that has expanded its traditional global distribution in the last decade. Recently, BTV-1 emerged in Southern Spain and caused several outbreaks in livestock reaching the north of the country. The aim of this paper was to review the emergence of BTV-1 in the Basque Country (Northern Spain) during 2007 and 2008 analyzing the possibility that infected *Culicoides* were introduced into Basque Country by winds from the infected areas of Southern Spain.

Methodology/Principal Findings: We use a complex HYSPLIT (Hybrid Single-Particle Lagrangian Integrated Trajectory) model to draw wind roses and backward wind trajectories. The analysis of winds showed September 28 to October 2 as the only period for the introduction of infected midges in the Basque Country. These wind trajectories crossed through the areas affected by serotype 1 on those dates in the South of the Iberian Peninsula. Additionally meteorological data, including wind speed and humidity, and altitude along the trajectories showed suitable conditions for *Culicoides* survival and dispersion.

Conclusions/Significance: An active infection in medium-long distance regions, wind with suitable speed, altitude and trajectory, and appropriate weather can lead to outbreaks of BTV-1 by transport of *Culicoides imicola*, not only over the sea (as reported previously) but also over the land. This shows that an additional factor has to be taken into account for the control of the disease which is currently essentially based on the assumption that midges will only spread the virus in a series of short hops. Moreover, the epidemiological and serological data cannot rule out the involvement of other *Culicoides* species in the spread of the infection, especially at a local level.

Citation: García-Lastra R, Leginagoikoa I, Plazaola JM, Ocabo B, Aduriz G, et al. (2012) Bluetongue Virus Serotype 1 Outbreak in the Basque Country (Northern Spain) 2007–2008. Data Support a Primary Vector Windborne Transport. PLoS ONE 7(3): e34421. doi:10.1371/journal.pone.0034421

Editor: Simon Gubbins, Institute for Animal Health, United Kingdom

Received: October 12, 2011; **Accepted:** February 28, 2012; **Published:** March 30, 2012

Copyright: © 2012 García-Lastra et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Funding: Funding for this work has been provided by the Dirección de Agricultura de the Departamento de Medio Ambiente, Planificación Territorial, Agricultura y Pesca of the Basque Government. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

* E-mail: rjuste@neiker.net

Introduction

Bluetongue (BT) is an arthropod-borne disease caused by a virus of the genus *Orbivirus*, the Bluetongue virus (BTV), which affects ruminant livestock such as cattle, sheep, and goats and wild ruminants such as deer, and camelids. Infected animals can show mild or no detectable clinical signs, but others can develop a clinical disease with signs ranging from fever, anorexia and weight loss, to nasal discharges, excessive salivation, edema of the lips, tongue and head, conjunctivitis, coronitis, lameness or abortions [1,2]. There are at least 26 BTV serotypes vectored by different species of midges of the genus *Culicoides* spp. depending on the geographic area and climatic factors [3].

Global distribution and recent emergence

Historically, BTV distribution across the world covered a broad band, approximately, between 40°N and 35°S, where BTV has

been enzootic throughout sub-Saharan Africa and wide areas of Asia and the Middle East. In Europe, and before 1998, outbreaks in Cyprus, the Iberian Peninsula and Greece were caused by brief sporadic incursions from adjacent enzootic regions and only with a single BTV serotype involved [4]. However, between 1998 and 2005, five serotypes of BTV (serotypes 1, 2, 4, 9 and 16) have been continuously present in the Mediterranean Basin, including several member states of the EU [5,6].

Thus, it seems that the global distribution of BTV infection has recently experienced an important change. Some authors have proposed that climate change is partially responsible for this modification in the BTV global distribution [7,8]. This fact could be explained by its impact on the vectorial capacity of resident *Culicoides* populations in previously virus-free regions such as much of the Mediterranean Basin. Nevertheless, the epidemiology of recent emergence of BTV-8 in Northern Europe would appear to be different from the spread of several BTV serotypes throughout